

***Streptococcus pneumoniae* Gateway®  
Clone Set, Recombinant in *Escherichia coli*, Plate 6****Catalog No. NR-19573**

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Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

**Manufacturer:**

BEI Resources

**Product Description:**

Clone plates are replicated using a BioMek® FX robot. Production in the 96-well format has increased risk of cross-contamination between adjacent wells. Individual clones should be purified (e.g. single colony isolation and purification using good microbiological practices) and sequence-verified prior to use. BEI Resources only confirms the clone plate orientation and viability of randomly picked clones. BEI Resources does not confirm or validate individual clone identities provided by the contributor.

The *Streptococcus pneumoniae* (*S. pneumoniae*) Gateway® clone set consists of approximately 2029 sequence validated clones from *S. pneumoniae*, strain TIGR4 cloned in *Escherichia coli* (*E. coli*) DH10B-T1 cells.<sup>1</sup> Each open reading frame was constructed in vector [pDONR™221](#) ([Invitrogen™](#)) with a native start codon and no stop codon. The sequence was validated by full length sequencing of each clone with greater than 1X coverage and a mutation rate of less than 0.2%. Detailed information about each clone is shown in Table 1.

Information related to the use of Gateway® Clones can be obtained from [Invitrogen™](#). Recombination was facilitated through an *attB* substrate (*attB*-PCR product or a linearized *attB* expression clone) with an *attP* substrate (pDONR™221) to create an *attL*-containing entry clone. The entry clone contains recombinational cloning sites, *attL1* and *attL2* to facilitate gene transfer into a destination vector, M13 forward and reverse priming sites for sequencing and a kanamycin resistance gene for selection. Please refer to the [Invitrogen™ Gateway® Technology Manual](#) for additional details.

**Material Provided:**

Each inoculated well of the 96-well plate contains approximately 60 µL of *E. coli* culture (strain DH10B-T1) in Luria Bertani (LB) broth containing 50 µg/mL kanamycin supplemented with 15% glycerol.

**Packaging/Storage:**

NR-19573 was packaged aseptically in a 96-well plate. The product is provided frozen and should be stored at -80°C or colder immediately upon arrival. For long-term storage, the vapor phase of a liquid nitrogen freezer is recommended. Freeze-thaw cycles should be avoided.

**Growth Conditions:**Media:

LB broth containing 50 µg/mL kanamycin

LB agar containing 50 µg/mL kanamycin

Incubation:

Temperature: 37°C.

Atmosphere: Aerobic

Propagation:

1. Scrape top of frozen well with a pipette tip and streak onto agar plate.
2. Incubate the plates at 37°C for 18 to 24 hours.

**Citation:**

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: *Streptococcus pneumoniae* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 6, NR-19573."

**Biosafety Level: 1**

Appropriate safety procedures should always be used with this material. Laboratory safety is discussed in the following publication: U.S. Department of Health and Human Services, Public Health Service, Centers for Disease Control and Prevention, and National Institutes of Health. [Biosafety in Microbiological and Biomedical Laboratories](#), 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see [www.cdc.gov/biosafety/publications/bmb15/index.htm](http://www.cdc.gov/biosafety/publications/bmb15/index.htm).

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**References:**

1. Kwon, K., et al. "A Correlation Analysis of Protein Characteristics Associated with Genome-Wide High Throughput Expression and Solubility of *Streptococcus pneumoniae* Proteins." *Protein Expr. Purif.* 55 (2007): 368-378. PubMed: 17703947.

ATCC® is a trademark of the American Type Culture Collection.



**Table 1: *Streptococcus pneumoniae* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 6 (YSPCF)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22905	A01	SP0133	hypothetical protein SP_0133	243	NP_344676.1	12.92593
22906	A02	SP0694	hypothetical protein SP_0694	690	NP_345199.1	11.98116
22907	A03	SP0488	hypothetical protein SP_0488	534	NP_345006.1	5.627341
22910	A04	SP1096	hypothetical protein SP_1096	1068	NP_345568.1	9.949438
22911	A05	SP0953	acetyltransferase	915	NP_345434.1	9.130055
22912	A06	SP0191	hypothetical protein SP_0190	291	NP_344732.1	5.175258
22913	A07	SP1875	segregation and condensation protein B	436	NP_346307.1	2
22914	A08	SP0153	hypothetical protein SP_0153	258	NP_344695.1	13.8876
22915	A09	SP0005	peptidyl-tRNA hydrolase	96	NP_344558.1	-
22916	A10	SP0260	hypothetical protein SP_0260	345	NP_344798.1	3.701449
22917	A11	SP2105	hypothetical protein SP_2105	1426	NP_346524.1	2.48317
22918	A12	SP1802	hypothetical protein SP_1802	193	NP_346235.1	2
22919	B01	SP0805	HAD superfamily hydrolase	777	NP_345302.1	8.124839
22920	B02	SP1793	hypothetical protein SP_1793	172	NP_346226.1	1.988372
22921	B03	SP1583	isochorismatase family protein	364	NP_346029.1	3.934066
22923	B04	SP0624	hypothetical protein SP_0624	633	NP_345136.1	5.315956
22925	B05	SP1847	xanthine phosphoribosyltransferase	313	NP_346279.1	2
22926	B06	SP1467	glutamine amidotransferase subunit PdxT	151	NP_345921.1	2
22927	B07	SP1233	hypothetical protein SP_1233	1254	NP_345699.1	9.307815
22928	B08	SP1320	v-type sodium ATP synthase, subunit E	1344	NP_345778.1	12.0439
22930	B09	SP0957	ABC transporter ATP-binding protein	918	NP_345438.1	7.867102
63466	B10	SP1332	hypothetical protein SP_1332	1398	NP_345790.1	21.34764
22932	B11	SP2182	hypothetical protein SP_2182	2002	NP_346593.1	3.803197
22933	B12	SP0107	LysM domain-containing protein	231	NP_344654.1	16.91775
22935	C01	SP1568	ribosome biogenesis GTP-binding protein YsxC	289	NP_346015.1	2
22936	C02	SP0331	hypothetical protein	399	-	2.897243
22937	C03	SP0746	ATP-dependent Clp protease proteolytic subunit	726	NP_345245.1	10.46281
22938	C04	SP0841	hypothetical protein SP_0841	813	NP_345332.1	7.483395
22941	C05	SP0099	hypothetical protein SP_0099	225	NP_344646.1	2
22942	C06	SP0567	hypothetical protein SP_0567	597	NP_345083.1	2.60469
22943	C07	SP1746	hypothetical protein SP_1746	1318	NP_346182.1	3.287557
22945	C08	SP2046	methyltransferase	1204	-	1.373754
22947	C09	SP1672	recombination protein RecR	814	NP_346111.1	3.918919
22948	C10	SP1204	hemolysin A	1215	NP_345671.1	6.618107

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22950	C11	SP1022	Sua5/YciO/YrdC family protein	978	NP_345497.1	8.635992
22951	C12	SP1813	N-(5'-phosphoribosyl)anthranilate isomerase	214	NP_346246.1	2
22953	D01	SP2000	DNA-binding response regulator	901	NP_346427.1	1.963374
22955	D02	SP0493	DNA-directed RNA polymerase subunit delta	537	NP_345011.3	5.960894
22956	D03	SP1880	deoxyribonucleotide triphosphate pyrophosphatase/unknown domain fusion protein	454	NP_346312.3	2
22957	D04	SP0622	nitroreductase family protein	630	NP_345134.1	3.461905
22958	D05	SP1471	oxidoreductase,	154	NP_345925.1	3
22959	D06	SP0971	dephospho-CoA kinase	927	NP_345452.1	8.952535
22960	D07	SP0766	superoxide dismutase, manganese-dependent	747	NP_345264.1	6.635877
22961	D08	SP1752	mechanosensitive ion channel	1408	NP_346188.1	2.944602
22962	D09	SP1925	hypothetical protein SP_1925	673	NP_346353.1	2
22963	D10	SP1492	cell wall surface anchor family protein	166	NP_345944.1	4
22964	D11	SP1804	general stress protein 24	196	NP_346237.1	2
22965	D12	SP1315	V-type ATP synthase subunit D	1344	NP_345773.1	12.90625
22966	E01	SP0085	30S ribosomal protein S4	204	NP_344633.1	2.897059
22968	E02	SP0547	hypothetical protein SP_0547	579	NP_345064.1	4.127807
22969	E03	SP1669	MutT/nudix family protein	793	NP_346108.1	4.630517
22970	E04	SP1456	peptide deformylase	139	NP_345910.1	4
22971	E05	SP1026	hypothetical protein SP_1026	984	NP_345501.1	8.880081
22973	E06	SP0154	hypothetical protein SP_0154	258	NP_344696.1	13.35659
22974	E07	SP0402	signal peptidase I	468	NP_344925.1	4.799145
22976	E08	SP1406	hypothetical protein SP_1406	1815	NP_345864.1	13.86556
22977	E09	SP0666	hypothetical protein SP_0666	660	NP_345171.1	4.125758
22978	E10	SP1522	hypothetical protein SP_1522	199	NP_345972.1	3
22979	E11	SP1720	hypothetical protein SP_1720	1054	NP_346157.1	3.074004
22981	E12	SP1945	hypothetical protein SP_1945	760	NP_346373.1	2
22983	F01	SP0984	phosphoglycerate mutase family protein	939	NP_345463.1	8.84345
22984	F02	SP2064	HAD superfamily hydrolase	1294	NP_346487.1	3.97527
22985	F03	SP0711	amino acid ABC transporter permease	696	NP_345213.1	12.63218
22986	F04	SP0315	-	378	-	3.296296
22987	F05	SP0026	hypothetical protein SP_0026	105	NP_344577.1	-
22988	F06	SP0673	hypothetical protein SP_0673	669	NP_345178.1	3.834081
22989	F07	SP0210	50S ribosomal protein L4	300	NP_344750.1	3.29
22990	F08	SP2039	hypothetical protein SP_2039	1138	NP_346464.1	1.507909
22991	F09	SP0209	50S ribosomal protein L3	300	NP_344749.1	3.706667
22992	F10	SP1738	guanylate kinase	1219	NP_346174.1	1.907301
22993	F11	SP1910	hypothetical protein SP_1910	571	NP_346339.1	2
22994	F12	SP0898	-	861	-	9.321719
22995	G01	SP1279	endonuclease III	1320	NP_345743.1	12.72424
22998	G02	SP1646	metallo-beta-lactamase superfamily protein	685	NP_346086.1	4.624818
22999	G03	SP1501	amino acid ABC transporter ATP-binding protein	181	NP_345952.1	3
23000	G04	SP0718	thiamine-phosphate pyrophosphorylase	702	NP_345219.1	13.70085
23001	G05	SP1436	hypothetical protein SP_1436	127	NP_345892.1	4
23002	G06	SP1747	nicotinic acid mononucleotide adenylyltransferase	1318	NP_346183.1	3.650986

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23003	G07	SP0745	uracil phosphoribosyltransferase	726	NP_345244.1	13.65978
23004	G08	SP0317	keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate aldolase	384	NP_344853.1	3.25
23006	G09	SP1627	hypothetical protein SP_1627	625	NP_346067.1	5.3616
23010	G10	SP0702	orotate phosphoribosyltransferase	690	NP_345205.1	13.11594
23013	G11	SP1260	copper homeostasis protein CutC	1281	NP_345724.1	13.31616
23014	G12	SP1450	platelet activating factor	136	NP_345904.1	4
23015	H01	SP0069	choline binding protein I	195	NP_344618.1	2.969231
23017	H02	SP2209	hypothetical protein SP_2209	2128	NP_346620.1	2.878289
23019	H03	SP0177	riboflavin synthase subunit alpha	279	NP_344718.1	4.354839
23020	H04	SP0350	capsular polysaccharide biosynthesis protein Cps4E	426	NP_344883.1	2.852113
23022	H05	SP1208	uridine kinase	1221	NP_345675.1	6.607699
23023	H06	SP0231	adenylate kinase	315	NP_344771.1	4.634921
23024	H07	SP0935	thymidylate kinase	888	NP_345419.1	8.208333
23026	H08	SP1705	hypothetical protein SP_1705	952	NP_346143.1	4.453782
23027	H09	SP0111	amino acid ABC transporter ATP-binding protein	231	NP_344658.1	13.74459
23028	H10	SP1090	redox-sensing transcriptional repressor Rex	1056	NP_345562.1	9.483902
23029	H11	SP2116	hypothetical protein SP_2116	1510	NP_346535.1	3.606623
23030	H12	SP1502	amino acid ABC transporter permease	181	NP_345953.1	4

<sup>1</sup>All information in this table was provided by J. Craig Venter Institute at the time of deposition.